

10 30 50
 CATGGGTGGGGGTGGGGGCGCTGCTGGATTCTGCTCTGGTGGAGGGGAACTTGTGAGG
 70 90 110
 GGCTGGTAAGCGCCCCCTCCGAAGCCTGGTGTGTGCGCGGGGGAAGGAAGTTAGTTTCC
 130 150 170
 TCTCCACCCATGGGCACCCCTTCTGCCCGGGGCTGGGAAGTGGGCTGCTCTGTGGGCAA
 190 210 230
 ATGCTGGGGCCTCTGAAATGGAGGAGACGCAGCAGGGAGAGGCCCCACGTGGGCAGCTGC
 M E E T Q Q G E A P R G O L R
 250 270 290
 GCGGAGAGTCAGCAGCACTGTCCCCCAGGCGCTCCTCCTGGTGTGCTGGGGGCCCGGG
 G E S A A P V P Q A L L L V L L G A R A
 310 330 350
 CCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAAGTCCACAAGAAGATTG
 Q G G T R S P R C D C A G D F H K K I G
 370 390 410
 GTCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGCACGGAGC
 L F C C R G C P A G H Y L K A P C T E P
 430 450 470
 CCTGCGGCAACTCCACCTGCCTTGTGTGTCCCAAGACACCTTCTTGGCCTGGGAGAACC
 C G N S T C L V C P Q D T F L A W E N H
 490 510 530
 ACCATAATTCTGAATGTGCCCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGTGGCGC
 H N S E C A R C Q A C D E Q A S Q V A L
 550 570 590
 TGGAGAAGTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGTGG
 E N C S A V A D T R C G C K P G W F V E
 610 630 650
 AGTGCCAGGTGAGCCAAATGTGTGTCAGCAGTTTACCCTTCTACTGCCAACCATGCCTAGACT
 C Q V S Q C V S S S P F Y C Q P C L D C
 670 690 710
 GCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGATACTGACTGTGGGA
 G A L H R H T R L L C S R R D T D C G T
 730 750 770
 CCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCCCCACGAGCACCC
 C L P G F Y E H G D G C V S C P T S T L
 790 810 830
 TGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGCAGATGTTCTGGGTCC
 G S C P E R C A A V C G W R Q M F W V O
 850 870 890
 AGGTGCTCCTGGCTGGCCTTGTGGTCCCCCTCCTGCTTGGGGCCACCCTGACCTACACAT
 V L L A G L V V P L L L G A T L T Y T Y
 910 930 950
 ACCGCCACTGCTGGCCTCACAAGCCCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCTC
 R H C W P H K P L V T A D E A G M E A L

FIGURE 1A

970 990 1010
 TGACCCACACCGGCCACCCATCTGTACCCCTTGGACAGCGCCACACCCCTTCTAGCAC
 T P P P A T H L S P L D S A H T L L A P

1030 1050 1070
 CTCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTAACAGCTGGACCCCTG
 P D S S E K I C T V Q L V G N S W T P G

1090 1110 1130
 GCTACCCCGAGACCCAGGAGGCGCTCTGCCCGCAGGTGACATGGTCCTGGGACCAGTTGC
 Y P E T Q E A L C P Q V T W S W D Q L P

1150 1170 1190
 CCAGCAGAGCTCTTGGCCCCGCTGTGCGCCCACTCTCGCCAGAGTCCCCAGCCGGCT
 S R A L G P A A A P T L S P E S P A G S

1210 1230 1250
 CGCCAGCATGATGCTGCAGCCGGGCGCGCAGCTCTACGACGTGATGGACGCGGTCCAG
 P A M M L Q P G P Q L Y D V M D A Y P A

1270 1290 1310
 CGCGGCGCTGGAAGGAGTTCTGTCGCGCAGCTGGGGCTGCGCGAGGCAGATCGAAGCCG
R R W K E F V R T L G L R E A E I E A V

1330 1350 1370
 TGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCC
E V E I G R F R D O O Y E M L K R W R O

1390 1410 1430
 AGCAGCAGCCCCGCGGCCCTCGGAGCCGTTTACGCGGCCCTGGAGCGCATGGGGCTGGACG
O O P A G L G A V Y A A L E R M G L D G

1450 1470 1490
 GCTGCGTGGAAGACTTGCGCAGCCGCTGCGAGCGGCGCCGTGACACGGCGCCCACTTGC
C V E D L R S R L Q R G P *

1510 1530 1550
 CACCTAGGCGCTCTGGTGGCCCTTGCAGAAGCCCTAAGTACGGTTACTTATGCGTGTAGA

1570 1590 1610
 CATTTTATGTCACTTATTAAGCCGCTGGCACGGCCCTGCGTAGCAGCACCAGCCGGCCCC

1630 1650 1670
 ACCCCTGCTCGCCCCTATCGCTCCAGCCAAGGCGAAGAAGCACGAACGAATGTCGAGAGG

1690 1710 1730
 GGGTGAAGACATTTCTCAACTTCTCGGCCGGAGTTTGGCTGAGATCGCGGTATTAAATCT

1750 1770
 GTGAAAGAAAACAAAACAAAACAAAAAAAAAAAAAAAAAAAAA

FIGURE 1B

1 ATGGAGCAGC GGCCGCGGGG CTGCGCGGCG GTGGCGGCGG CGCTCCTCCT GGTGCTGCTG
 M E Q R P R G C A A V A A A L L L V L L
 61 GGGGCCCCGG CCCAGGGCGG CACTCGTAGC CCCAGGTGTG ACTGTGCCGG TGAATTCCAC
 G A R A Q G G T R S P R C D C A G D F H
 121 AAGAAGATTG GTCTGTTTGT TTGCAGAGGC TGCCCGAGCG GGAAGTACCT GAAGGCCCTT
 K K I G L F C C R G C P A G H Y L K A P
 181 TGCACGGAGC CCTGCGGCAA CTCCACCTGC CTTGTGTGTC CCCAAGACAC CTTCTTGGCC
 C T E P C G N S T C L V C P Q D T F L A
 241 TGGGAGAACC ACCATAATTC TGAATGTGCC CGCTGCCAGG CCTGTGATGA GCAGGCCTCC
 W E N H H N S E C A R C Q A C D E Q A S
 301 CAGGTGGCGC TGGAGAACTG TTCAGCAGTG GCCGACACCC GCTGTGGCTG TAAGCCAGGC
 Q V A L E N C S A V A D T R C G C K P G
 361 TGGTTTGTGG AGTGCCAGGT CAGCCAATGT GTCAGCAGTT CACCCTTCTA CTGCCAACCA
 W F V E C Q V S Q C V S S S P F Y C Q P
 421 TGCCTAGACT GCGGGGCCCT GCACCGCCAC ACACGGCTAC TCTGTTCCCG CAGAGATACT
 C L D C G A L H R H T R L L C S R R D T
 481 GACTGTGGGA CCTGCCTGCC TGGCTTCTAT GAACATGGCG ATGGCTGCGT GTCCTGCCCC
 D C G T C L P G F Y E H G D G C V S C P
 541 ACGAGCACCC TGGGGAGCTG TCCAGAGCGC TGTGCCGCTG TCTGTGGCTG GAGGCAGATG
 T S T L G S C P E R C A A V C G W R Q M
 601 TTCTGGGTCC AGGTGCTCCT GGCTGGCCTT GTGGTCCCCC TCCTGCTTGG GGCCACCCTG
 F W V Q V L L A G L V V P L L L G A T L
 661 ACCTACACAT ACCGCCACTG CTGGCCTCAC AAGCCCCCTG TTACTGCAGA TGAAGCTGGG
 T Y T Y R H C W P H K P L V T A D E A G
 721 ATGGAGGCTC TGACCCACCC ACCGGCCACC CATCTGTCAC CCTTGGACAG CGCCACACC
 M E A L T P P P A T H L S P L D S A H T
 781 CTTCTAGCAC CTCCTGACAG CAGTGAGAAG ATCTGCACCG TCCAGTTGGT GGGTAACAGC
 L L A P P D S S E K I C T V Q L V G N S
 841 TGGACCCCTG GCTACCCCGA GACCCAGGAG GCGCTCTGCC CGCAGGTGAC ATGGTCCCTG
 W T P G Y P E T Q E A L C P Q V T W S W
 901 GACCAGTTGC CCAGCAGAGC TCTTGGCCCC GCTGCTGCGC CCACACTCTC GCCAGAGTCC
 D Q L P S R A L G P A A A P T L S P E S
 961 CCAGCCGGCT CGCCAGCCAT GATGCTGCAG CCGGGCCCGC AGCTCTACGA CGTGATGGAC
 P A G S P A M M L Q P G P Q L Y D V M D
 1021 GCGGTCCCAG CGCGGCGCTG GAAGGAGTTC GTGCGCACGC TGGGGCTGCG CGAGGCAGAG
 A V P A R R W K E F V R T L G L R E A E
 1081 ATCGAAGCCG TGGAGGTGGA GATCGGCCGC TTCCGAGACC AGCAGTACGA GATGCTCAAG
 I E A V E V E I G R F R D Q Q Y E M L K
 1141 CGCTGGCGCC AGCAGCAGCC CGCGGGCCTC GGAGCCGTTT ACGCGGCCCT GGAGCGCATG
 R W R Q Q Q P A G L G A V Y A A L E R M
 1201 GGGCTGGACG GCTGCGTGGA AGACTTGCGC AGCCGCTGC AGCGCGGCC GTGA
 G L D G C V E D L R S R L Q R G P

FIGURE 2

Consensus #1	M	
DDCR	M E E T Q Q G E A P R G Q L R G E S A A P V P Q A L L L V L	30
TNFR1	M G L S T V P D L L L P L V L L E L L V G I Y P S G V I G L	30
FAS	M - L G I W T L L P L V L T S V A R L S S K S V N A Q V T D	29
Consensus #1 C	
DDCR	L G A R A Q G G T R S P R C D C A G D F H - - K K I G L F C	58
TNFR1	V P H L G D R E K R D S V C P Q G K Y I H - - P Q N N S I C	58
FAS	I N S K G L E L R K T V T T V E T Q N L E G L H H D G Q F C	59
Consensus #1	. . . C . . G C C . . C . . .	
DDCR	C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T	88
TNFR1	C T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G S	88
FAS	H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K	89
Consensus #1 H . . . C . . C . . C C	
DDCR	F L A W E N H H N S E C A R C Q A C D E Q A S Q V A L E N C	118
TNFR1	F T A S E N H L R - H C L S C S K C R K E M G Q V E I S S C	117
FAS	E Y T D K A H F S S K C R R C R L C D E G H G L E V E I N C	119
Consensus #1 T . C . C	
DDCR	S A V A D T R C G C K P G W F V E C - - - Q V S Q C V S S S	145
TNFR1	T V D R D T V C G C R K N Q Y R H Y W S E N L F Q C - - -	144
FAS	T R T Q N T K C R C K P N F F Q N - - - - - - - - - -	137
Consensus #1 C	
DDCR	P F Y C Q P C L D C G A L H R H T R L L C S R R D T D C G T	175
TNFR1	- F N C S L C L N - G T V H - - - L S C Q E K Q N T V C T	167
FAS	- - - S T V C E H C D P - - - - - - - - - - C T K	148
Consensus #1	C . . G C C . .	
DDCR	C L P G F Y E H G D G C V S C P T S T L G - S C P E R C - -	203
TNFR1	C H A G F F L R E N E C V S C S N C K K S L E C T K L C L P	197
FAS	C E H G I I - - - K E C - - - - - - - - - T L T S N T K C	166
Consensus #1 L	
DDCR	- - - - - A A V C G W R Q M F W V Q V L L A G L V V P L	225
TNFR1	Q I E N V K G T E D S G T T V L L P L V I F F G L C L L S L	227
FAS	- - - - - K E E G S R S N L G W L C L L L - - L P I P L	186
Consensus #1	
DDCR	L L G G T L D L H I P P L L A H K P L V T A D E A G M E A L	255
TNFR1	L F I G - L M Y R Y Q R W K S K L Y S I V C G K S T P E K E	256
FAS	I V - - - - - W V K R K E V - - - Q K T C R K H R	203
Consensus #1 G P	
DDCR	N P P P G T H L S P L D S A H T L L A P P D S S E K I C T V	285
TNFR1	G E L E G T T T K P L A P N P S F S P T P G F T P T L G F S	286
FAS	K E N Q G S H E S P - - - - - - - - - - - - -	214

FIGURE 3

Consensus #1

DDCR Q L V G N S W **T** P G Y P E **T** Q E A L **C** P Q V T W S W D Q L - 315
 TNFR1 P V P S S T F **T** S S S T Y **T** P G D - **C** P N F A A P R R E V A 315
 FAS - - - - - 214

Consensus #1 L

DDCR - **P** S R A L G **P** A A **A** P **T** L S **P** E S P **A** G S - - - - - 336
 TNFR1 P **P** Y Q G A D **P** I L **A** T A L A S D P I P N P **L** Q K W E D S A 345
 FAS - - - - - **T** L N **P** E T V **A** I N **L** S - - - - - 226

Consensus #1 K . F V

DDCR - - - P A M M L O P G P Q **L** Y D **V** M D A **V** P A R **R** W K E F V 362
 TNFR1 H K P Q S L **D** T **D** D P A T **L** Y A **V** V E N **V** P L **R** W K E F V 375
 FAS - - - - - **D** V **D** L S K Y I T T I A G V M T L S Q V **K** G E F V 249

Consensus #1 R . . G I L .

DDCR **R** T **L** G L R **E** A E I E A V **E** V E I C R - F **R** D Q Q Y E M L K 391
 TNFR1 **R** R **L** G L S D H E I D R L **E** L Q N C R C L **R** E A Q Y S M L A 405
 FAS **R** K N **G** V N **E** A K I D E I K N D **N** V Q D T A **E** Q K V Q L L R 279

Consensus #1 . W A L L E

DDCR R **W** R Q Q Q **P** - - - **A** G **L** G A V Y A A **L** E R M G **L** D **C** C V **E** 418
 TNFR1 T **W** R R R T **P** R R **E** A T **L** E L **L** G R V **L** R D M D **L** L **C** C L **E** 435
 FAS N **W** H **Q** L H G K K **E** A - Y D T **L** I K D **L** K K A N **L** C T L A **E** 308

Consensus #1

DDCR **D** L - - - - - R **S** R **L** Q R G **P** 428
 TNFR1 **D** T E E A L - - - - - C G P A A **L** P P A **P** S L **L** R 455
 FAS K **T** Q T I I L K D I T S D S E N **S** N F R N E I Q S **L** V 335

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIGURE 3 (CONT'D)

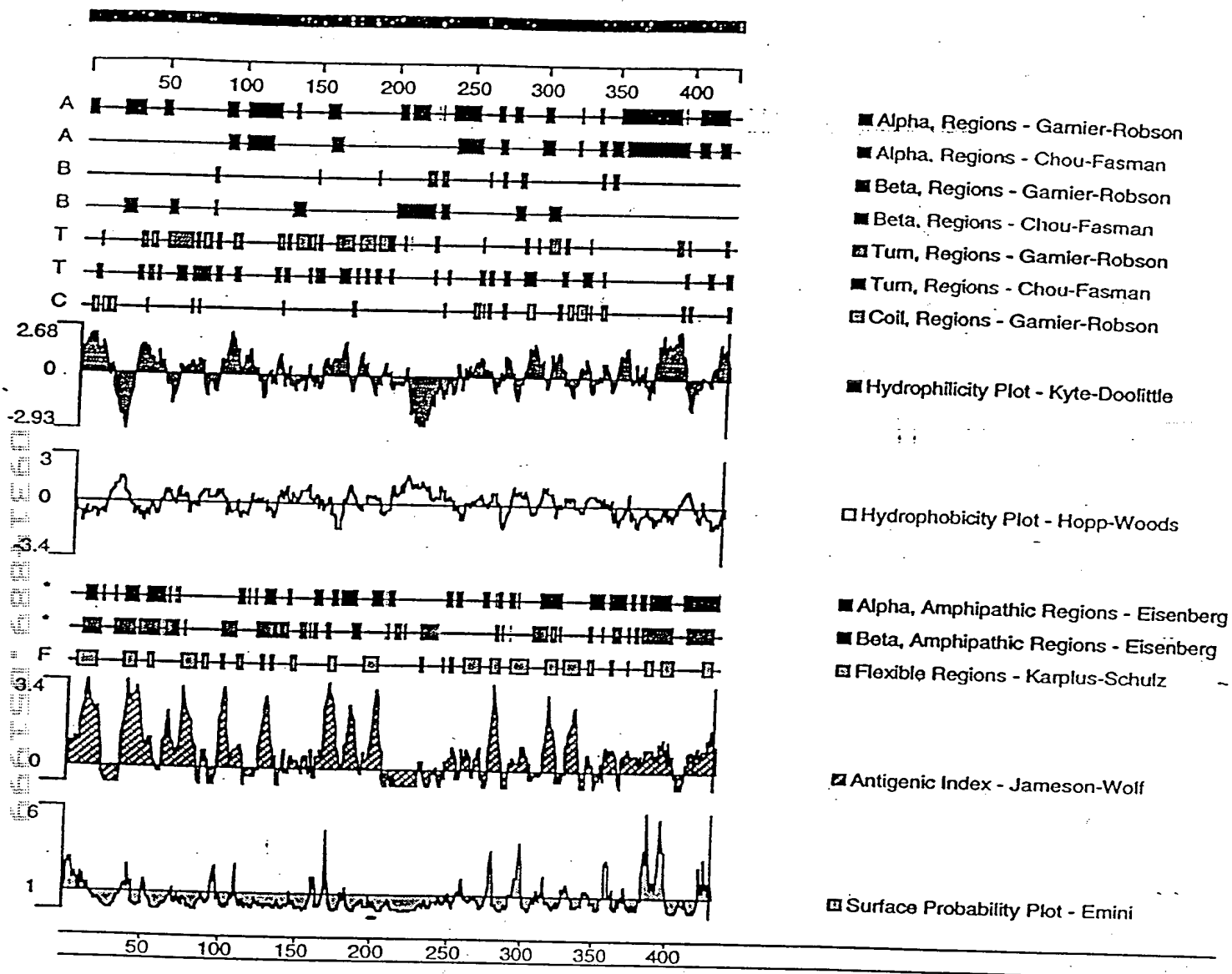


FIGURE 4